DT05 Rec'd PCT/PTO 2 1 OCT 2004

WO 03/089932

SEQUENCE LISTING

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						- 4-4-			~		ata	ata	ata	103
Phe Le	cc acc	ctg to Leu Se	er Val	acg Thr	Trp	Ile	Gly	Ala	Ala	Pro	Leu	Ile	Leu	103
		10			~	15	_				20			
tct c	gg att	gtg gg	ga ggc	tgg	gag	tgc	gag	aag	cat	tcc	caa	ccc	tgg	151
Ser A	rg Ile	Val Gl	ly Gly	Trp	Glu 30	Cys	Glu	Lys	His	Ser 35	Gln	Pro	Trp	
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cag g	tg ctt al Leu	gtg go	cc tct	cgt	ggc	agg	gca Mla	gtc Val	tgc	ggc	ggt	gtt Val	ctg Leu	199
4		val Al	la sei	45	GIY	ALG	AIG	vai	50	O.L.y	GIY	vai	Lea	
ata a	ac ccc	ana ta	a ata	ctc	202	act	acc	cac	tac	atc	add	aac	aaa	247
Val H	is Pro	Gln Ti	rp Val	Leu	Thr	Ala	Ala	His	Cys	Ile	Arg	Asn	Lys	21,
55			60					65					70	
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Ser V	al Ile	Leu Le	eu Gly	Arg	His	Ser	Leu	Phe	His	Pro	Glu	Asp	Thr	
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Gly G	ln Val	Phe Gi	ın Val	Ser	His	Ser 95	Phe	Pro	Hls	Pro	Leu 100	луr	Asp	
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met 3	cr nea	Ter ni	la van	$rac{1}{2}$	2 110	Lu	****		1	ىرى	_P			

110

105

115

103						
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gct gtg aag Ala Val Lys 135	gtc atg ga Val Met As	p Leu Pro	acc cag gag Thr Gln Glu 145	cca gca ctg Pro Ala Leu	ggg acc Gly Thr 150	487
acc tgc tac Thr Cys Tyr	gcc tca gg Ala Ser Gl 155	gc tgg ggc .y Trp Gly	agc att gaa Ser Ile Glu 160	cca gag gag Pro Glu Glu	tgt acg Cys Thr 165	535
cct ggg cca Pro Gly Pro	gat ggt go Asp Gly Al	a gcc ggg la Ala Gly	agc cca gat Ser Pro Asp 175	gcc tgg gtc Ala Trp Val 180		577
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tactgg						1603

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<211> 180

<212> PRT

<213> Human

<400> 2

Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly

Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu 25

Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala

Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala 55

His Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu 70

Phe His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe 85

Pro His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg 105 100

Pro Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu 120 115

Pro Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln 135 130

Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile 150 155

Glu Pro Glu Glu Cys Thr Pro Gly Pro Asp Gly Ala Ala Gly Ser Pro

Asp Ala Trp Val 180

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<213> Human

<220>

<221> CDS

<222> (1)..(489)

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cat His	tcc Ser	caa Gln	ccc Pro 20	tgg Trp	cag Gln	gtg Val	ctt Leu	gtg Val 25	gcc Ala	tct Ser	cgt Arg	ggc Gly	agg Arg 30	gca Ala	gtc Val	96
tgc Cys	ggc Gly	ggt Gly 35	gtt Val	ctg Leu	gtg Val	cac His	ccc Pro 40	cag Gln	tgg Trp	gtc Val	ctc Leu	aca Thr 45	gct Ala	gcc Ala	cac His	144
														ctg Leu		192
														ttc Phe		240
														agg Arg 95		288
ggt Gly	gat Asp	gac Asp	tcc Ser 100	agc Ser	cac His	gac Asp	ctc Leu	atg Met 105	ctg Leu	ctc Leu	cgc Arg	ctg Leu	tca Ser 110	gag Glu	cct Pro	336
gcc Ala	gag Glu	ctc Leu 115	acg Thr	gat Asp	gct Ala	gtg Val	aag Lys 120	gtc Val	atg Met	gac Asp	ctg Leu	ccc Pro 125	acc Thr	cag Gln	gag Glu	384
cca Pro	gca Ala 130	ctg Leu	gly aaa	acc Thr	acc Thr	tgc Cys 135	tac Tyr	gcc Ala	tca Ser	ggc	tgg Trp 140	ggc Gly	agc Ser	att Ile	gaa Glu	432
														cca Pro		480
		gtc Val	tga													. 492

<210> 4

<211> 163

<212> PRT

<213> Human

<400> 4

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1 10 15

His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val

Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His 35 40 45

Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu Phe 50 55 His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe Pro 75 70 His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg Pro 85 90 Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro 100 Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln Glu 120 Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu 135 Pro Glu Glu Cys Thr Pro Gly Pro Asp Gly Ala Ala Gly Ser Pro Asp 155 150 Ala Trp Val <210> 5 <211> 471 <212> DNA <213> Human <220> <221> CDS <222> (1)..(468) 48 att gtg gga ggc tgg gag tgc gag aag cat tcc caa ccc tgg cag gtg Ile Val Gly Gly Trp Glu Cys Glu Lys His Ser Gln Pro Trp Gln Val ctt gtg gcc tct cgt ggc agg gca gtc tgc ggc ggt gtt ctg gtg cac 96 Leu Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly Val Leu Val His 25 ccc cag tgg gtc ctc aca gct gcc cac tgc atc agg aac aaa agc gtg 144 Pro Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg Asn Lys Ser Val 35 40 192 atc ttg ctg ggt cgg cac agc ctg ttt cat cct gaa gac aca ggc cag Ile Leu Leu Gly Arg His Ser Leu Phe His Pro Glu Asp Thr Gly Gln 60 50 55

gta Val 65	ttt Phe	cag Gln	gtc Val	agc Ser	cac His 70	agc Ser	ttc Phe	cca Pro	cac His	ccg Pro 75	ctc Leu	tac Tyr	gat Asp	atg Met	agc Ser 80	240
ctc Leu	ctg Leu	aag Lys	aat Asn	cga Arg 85	ttc Phe	ctc Leu	agg Arg	cca Pro	ggt Gly 90	gat Asp	gac Asp	tcc Ser	agc Ser	cac His 95	gac Asp	288
ctc Leu	atg Met	ctg Leu	ctc Leu 100	cgc Arg	ctg Leu	tca Ser	gag Glu	cct Pro 105	gcc Ala	gag Glu	ctc Leu	acg Thr	gat Asp 110	gct Ala	gtg Val	336
aag Lys	gtc Val	atg Met 115	gac Asp	ctg Leu	ccc Pro	acc Thr	cag Gln 120	gag Glu	cca Pro	gca Ala	ctg Leu	999 Gly 125	acc Thr	acc Thr	tgc Cys	384
tac Tyr	gcc Ala 130	tca Ser	ggc	tgg Trp	ggc Gly	agc Ser 135	att Ile	gaa Glu	cca Pro	gag Glu	gag Glu 140	tgt Cys	acg Thr	cct Pro	gjå aaa	432
						agc Ser					gtc Val	tga				471
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<212> PRT <213> Human <400> 6

Ile Val Gly Gly Trp Glu Cys Glu Lys His Ser Gln Pro Trp Gln Val
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Leu Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly Val Leu Val His 20 25 30

Pro Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg Asn Lys Ser Val 35 40 45

Ile Leu Leu Gly Arg His Ser Leu Phe His Pro Glu Asp Thr Gly Gln 50 55 60

Val Phe Gln Val Ser His Ser Phe Pro His Pro Leu Tyr Asp Met Ser 65 70 75 80

Leu Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp Ser Ser His Asp 85 90 95

Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu Thr Asp Ala Val

Lys Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr Cys

115 120 125

Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu Cys Thr Pro Gly 130 135 140

Pro Asp Gly Ala Ala Gly Ser Pro Asp Ala Trp Val 145 150 155

<210> 7

<211> 708

<212> DNA

<213> Human

<220>

<221> misc feature

<222> (38)..(577)

<223> CDS

<400> 7

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<210> 8

<211> 16

<212> PRT

<213> Human

<400> 8

Cys Thr Pro Gly Pro Asp Gly Ala Ala Gly Ser Pro Asp Ala Trp Val 1 5 10 15

<210> 9

<211> 1541

<212> DNA <213> Human

<220> <221> CDS

<222> (17)..(685)

<400> 9

ggacacctgt gtcagc atg tgg gac ctg gtt ctc tcc atc gcc ttg tct gtg 52

Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val

1 5 10

ggg tgc act ggt gcc gtg ccc ctc atc cag tct cgg att gtg gga ggc 100 Gly Cys Thr Gly Ala Val Pro Leu Ile Gln Ser Arg Ile Val Gly

tgg gag tgt gag aag cat tcc caa ccc tgg cag gtg gct gtg tac agt

Trp Glu Cys Glu Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser

30 40

cat gga tgg gca cac tgt ggg ggt gtc ctg gtg cac ccc cag tgg gtg
His Gly Trp Ala His Cys Gly Gly Val Leu Val His Pro Gln Trp Val
45 50 55 60

ctc aca gct gcc cat tgc cta aag aag aat agc cag gtc tgg ctg ggt
Leu Thr Ala Ala His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly
65 70 75

cgg cac aac ctg ttt gag cct gaa gac aca ggc cag agg gtc cct gtc 292
Arg His Asn Leu Phe Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val
80 85 90

agc cac agc ttc cca cac ccg ctc tac aat atg agc ctt ctg aag cat

Ser His Ser Phe Pro His Pro Leu Tyr Asn Met Ser Leu Leu Lys His

95 100 105

caa agc ctt aga cca gat gaa gac tcc agc cat gac ctc atg ctg ctc 388
Gln Ser Leu Arg Pro Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu
110 115 120

cgc ctg tca gag cct gcc aag atc aca gat gtt gtg aag gtc ctg ggc
Arg Leu Ser Glu Pro Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly
125 130 135 140

ctg ccc acc cag gag cca gca ctg ggg acc acc tgc tac gcc tca ggc
Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly
145
150
155

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Trp Gly Ser Ile Glu Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln

160 165 170

tgt gtg agc ctc cat ctc ctg tcc aat gac atg tgt gct aga gct tac

Cys Val Ser Leu His Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr

175

180

580

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Ser Glu Lys Val Thr Glu Phe Met Leu Cys Ala Gly Leu Trp Thr Gly
190 . 195 200

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<211> 223 <212> PRT <213> Human

<400> 10

Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val Gly Cys Thr Gly

Ala Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu 25

Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala 35

His Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala 50 55 60

His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu

65 70 75 80

Phe Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val Ser His Ser Phe 85 90 95

Pro His Pro Leu Tyr Asn Met Ser Leu Leu Lys His Gln Ser Leu Arg 100 105 110

Pro Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
115 120 125

Pro Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln
130 135 140

Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile 145 150 155 160

Glu Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln Cys Val Ser Leu 165 170 175

His Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr Ser Glu Lys Val 180 185 190

Thr Glu Phe Met Leu Cys Ala Gly Leu Trp Thr Gly Gly Lys Asp Thr 195 200 205

Cys Gly Val Ser His Pro Tyr Ser Gln His Leu Glu Gly Lys Gly 210 215 220

<210> 11

<211> 621

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)..(618)

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cat tcc caa ccc tgg cag gtg gct gtg tac agt cat gga tgg gca cac 96
His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala His
20 25 30

tgt ggg ggt gtc ctg gtg cac ccc cag tgg gtg ctc aca gct gcc cat

Cys Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His

35

40

45

tgc Cys	cta Leu 50	aag Lys	aag Lys	aat Asn	agc Ser	cag Gln 55	gtc Val	tgg Trp	ctg Leu	ggt Gly	cgg Arg 60	cac His	aac Asn	ctg Leu	ttt Phe	192
gag Glu 65	cct Pro	gaa Glu	gac Asp	aca Thr	ggc Gly 70	cag Gln	agg Arg	gtc Val	.cct Pro	gtc Val 75	agc Ser	cac His	agc Ser	ttc Phe	cca Pro 80	240
									aag Lys 90							288
									ctg Leu							336
gcc Ala	aag Lys	atc Ile 115	aca Thr	gat Asp	gtt Val	gtg Val	aag Lys 120	gtc Val	ctg Leu	ggc Gly	ctg Leu	ccc Pro 125	acc Thr	cag Gln	gag Glu	384
									tca Ser							432
cca Pro 145	gag Glu	gag Glu	ttc Phe	ttg Leu	cgc Arg 150	ccc Pro	agg Arg	agt Ser	ctt Leu	cag Gln 155	tgt Cys	gtg Val	agc Ser	ctc Leu	cat His 160	480
ctc Leu	ctg Leu	tcc Ser	aat Asn	gac Asp 165	atg Met	tgt Cys	gct Ala	aga Arg	gct Ala 170	tac Tyr	tct Ser	gag Glu	aag Lys	gtg Val 175	aca Thr	528
gag Glu	ttc Phe	atg Met	ttg Leu 180	tgt Cys	gct Ala	gly	ctc Leu	tgg Trp 185	aca Thr	ggt Gly	ggt Gly	aaa Lys	gac Asp 190	act Thr	tgt Cys	576
									ctg Leu					tga		621

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<211> 206

<212> PRT

<213> Human

<400> 12

Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Lys
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His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala His 20 25 30

Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His 35 40 45

Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu Phe 50 55 60

Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val Ser His Ser Phe Pro 65 70 75 80

His Pro Leu Tyr Asn Met Ser Leu Leu Lys His Gln Ser Leu Arg Pro 85 90 95

Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro 100 105 110

Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln Glu 115 120 125

Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu 130 135 140

Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln Cys Val Ser Leu His 145 150 155 160

Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr Ser Glu Lys Val Thr
165 170 175

Glu Phe Met Leu Cys Ala Gly Leu Trp Thr Gly Gly Lys Asp Thr Cys 180 185 190

Gly Val Ser His Pro Tyr Ser Gln His Leu Glu Gly Lys Gly 195 200 205

<210> 13

<211> 600

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)..(597)

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Ala Val Tyr Ser His Gly Trp Ala His Cys Gly Gly Val Leu Val His
20 25 30

ccc cag tgg gtg ctc aca gct gcc cat tgc cta aag aag aat agc cag
Pro Gln Trp Val Leu Thr Ala Ala His Cys Leu Lys Lys Asn Ser Gln

40 45 35 gtc tgg ctg ggt cgg cac aac ctg ttt gag cct gaa gac aca ggc cag 192 Val Trp Leu Gly Arg His Asn Leu Phe Glu Pro Glu Asp Thr Gly Gln 240 agg gtc cct gtc agc cac agc ttc cca cac ccg ctc tac aat atg agc Arq Val Pro Val Ser His Ser Phe Pro His Pro Leu Tyr Asn Met Ser ctt ctg aag cat caa agc ctt aga cca gat gaa gac tcc agc cat gac 288 Leu Leu Lys His Gln Ser Leu Arg Pro Asp Glu Asp Ser Ser His Asp 336 ctc atg ctg ctc cgc ctg tca gag cct gcc aag atc aca gat gtt gtg Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Lys Ile Thr Asp Val Val 105 100 aag gtc ctg ggc ctg ccc acc cag gag cca gca ctg ggg acc acc tgc 384 Lys Val Leu Gly Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr Cys 125 120 432 tac gcc tca ggc tgg ggc agc atc gaa cca gag gag ttc ttg cgc ccc Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu Phe Leu Arg Pro 135 130 480 agg agt ctt cag tgt gtg agc ctc cat ctc ctg tcc aat gac atg tgt Arg Ser Leu Gln Cys Val Ser Leu His Leu Leu Ser Asn Asp Met Cys 155 150 145 gct aga gct tac tct gag aag gtg aca gag ttc atg ttg tgt gct ggg 528 Ala Arg Ala Tyr Ser Glu Lys Val Thr Glu Phe Met Leu Cys Ala Gly 165 170 ctc tgg aca ggt ggt aaa gac act tgt ggg gtg agt cat ccc tac tcc 576 Leu Trp Thr Gly Gly Lys Asp Thr Cys Gly Val Ser His Pro Tyr Ser 185 180

caa cat ctg gag ggg aaa ggg tga 600 Gln His Leu Glu Gly Lys Gly 195

<210> 14 <211> 199

<212> PRT

<213> Human

<400> 14

Ile Val Gly Gly Trp Glu Cys Glu Lys His Ser Gln Pro Trp Gln Val
5 10 15

Ala Val Tyr Ser His Gly Trp Ala His Cys Gly Gly Val Leu Val His 20 25 30

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Arg Val Pro Val Ser His Ser Phe Pro His Pro Leu Tyr Asn Met Ser 65 70 75 80

Leu Leu Lys His Gln Ser Leu Arg Pro Asp Glu Asp Ser Ser His Asp 85 90 95

Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Lys Ile Thr Asp Val Val 100 105 110

Lys Val Leu Gly Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr Cys 115 120 125

Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu Phe Leu Arg Pro 130 135 140

Arg Ser Leu Gln Cys Val Ser Leu His Leu Leu Ser Asn Asp Met Cys 145 150 155 160

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PCT/AU03/00454

WO 03/089932

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PCT/AU03/00454

WO 03/089932